

FIG 1

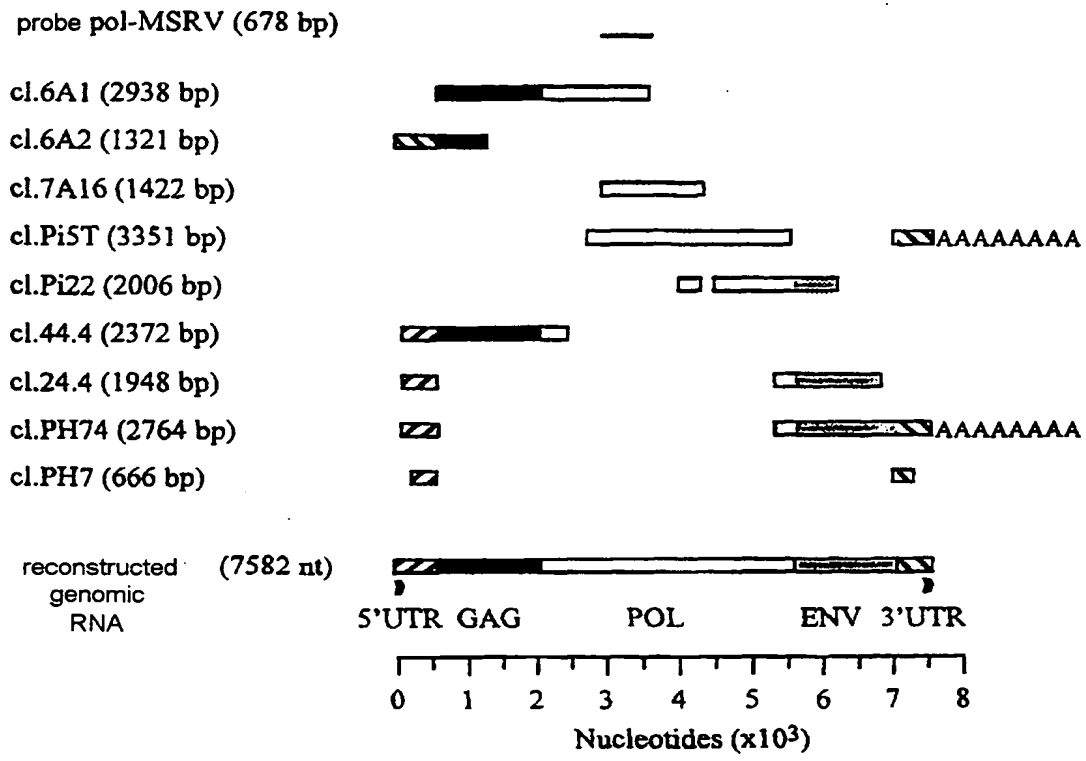


Diagram illustrating the organization of the P5' region of the Penv-C15 genome. The diagram shows the DNA sequence (RG083M05) and the corresponding RNA sequences (Putative genomic mRNA, c1.PH74, c1.PH7, c1.Pi5T) with their respective 5' and 3' ends. The DNA sequence is divided into three regions: AS1, AS2, and AS3. The RNA sequences are also divided into three regions: R-U5, R-U5, and R. The diagram shows the relative positions of the 5' and 3' ends of the RNA sequences and the DNA sequence. The DNA sequence is shown as a double-stranded molecule with the top strand (coding strand) and the bottom strand (template strand). The RNA sequences are shown as single-stranded molecules. The diagram illustrates the organization of the P5' region of the Penv-C15 genome, showing the DNA sequence and the corresponding RNA sequences.

Probes

P5' env-cl.24.4	Pgag-LB19 Ppro-E Ppol-MSRV	Penv-C15
atccaaagtgtgagtaata ATCCAAAGTG	caggaggaaagtaactaaaa CAGGAGGAAAGTAACTAAAA	
cttttttcagatgggaaacg ATCGGAACG	ccatccctagatacatctctg CATCCCTAGTACATCTTG	tctcttccagaatogaagct TCTCTCCAGATOGAGCT

Probes

FIG 3

	Names	Similarities	Repetitions	ORFs
1	Recons RNA		yes	538
28274	RG083M05 [7]	96%	yes	538
6911	BAC378 [14]	88%	yes	no
35199	Q11M15 [21]	89%	yes	413 and 305
91299	U134E6 [x]	88%	no	no

1kB

FIG 4A

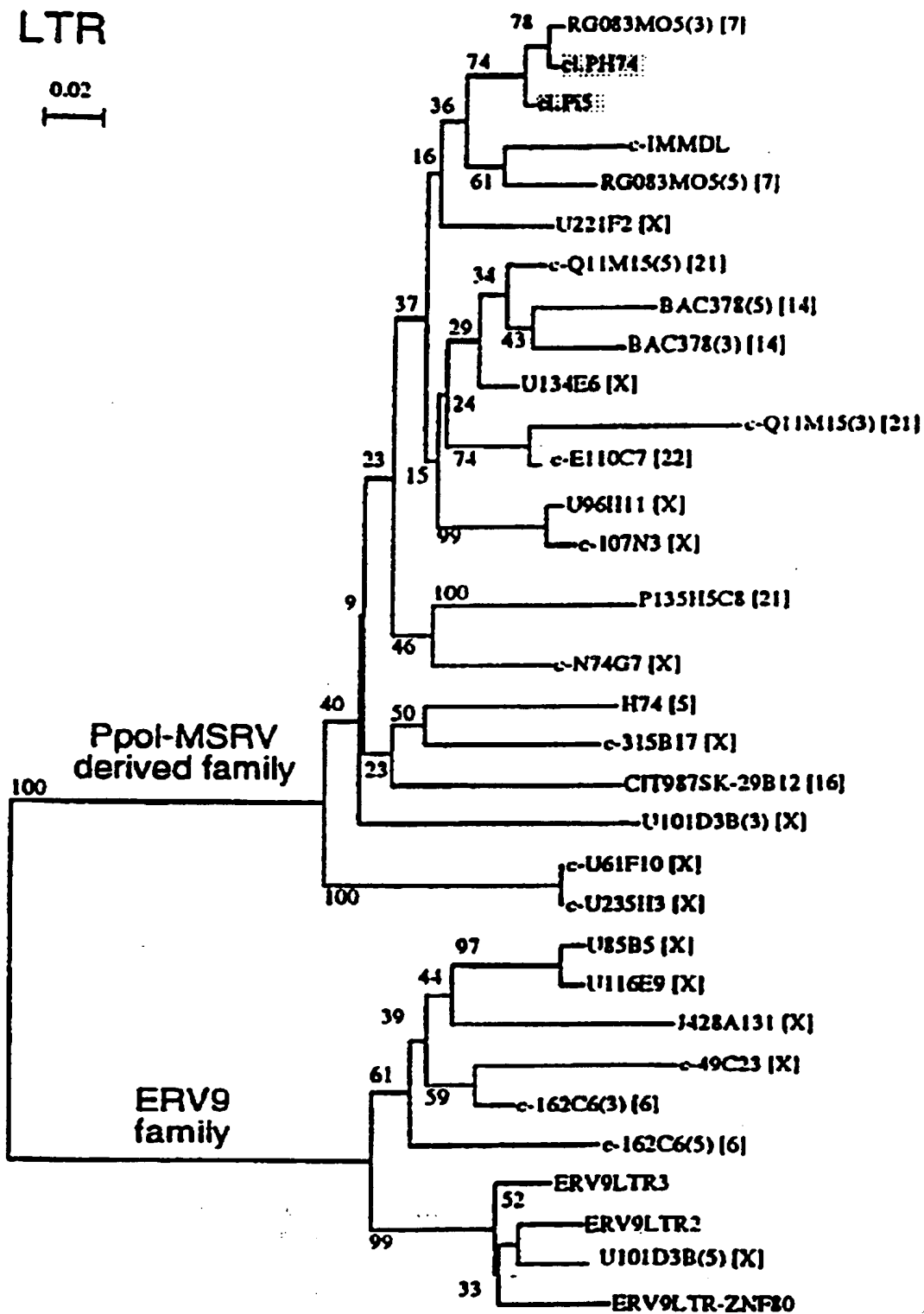


FIG 4 B

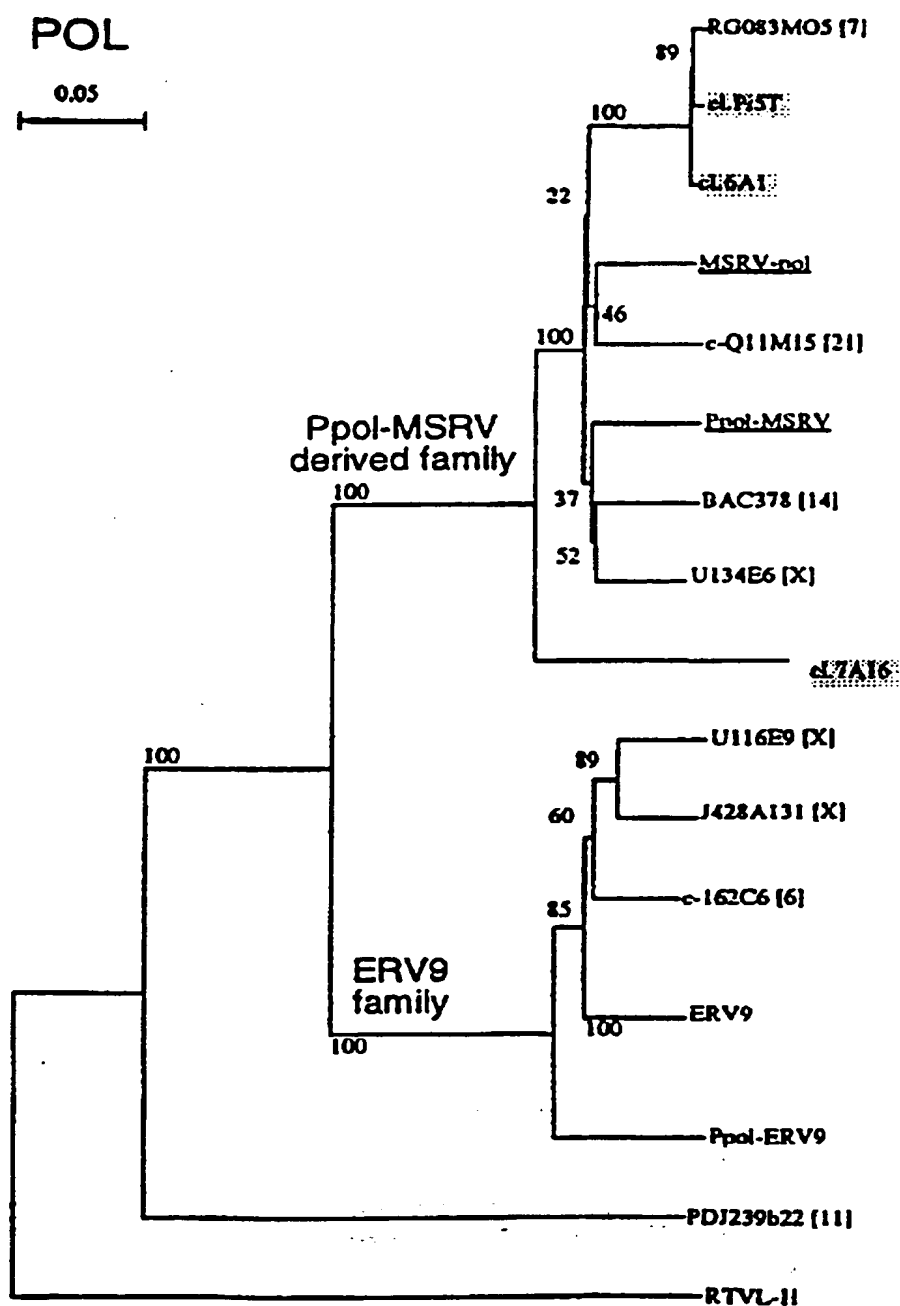
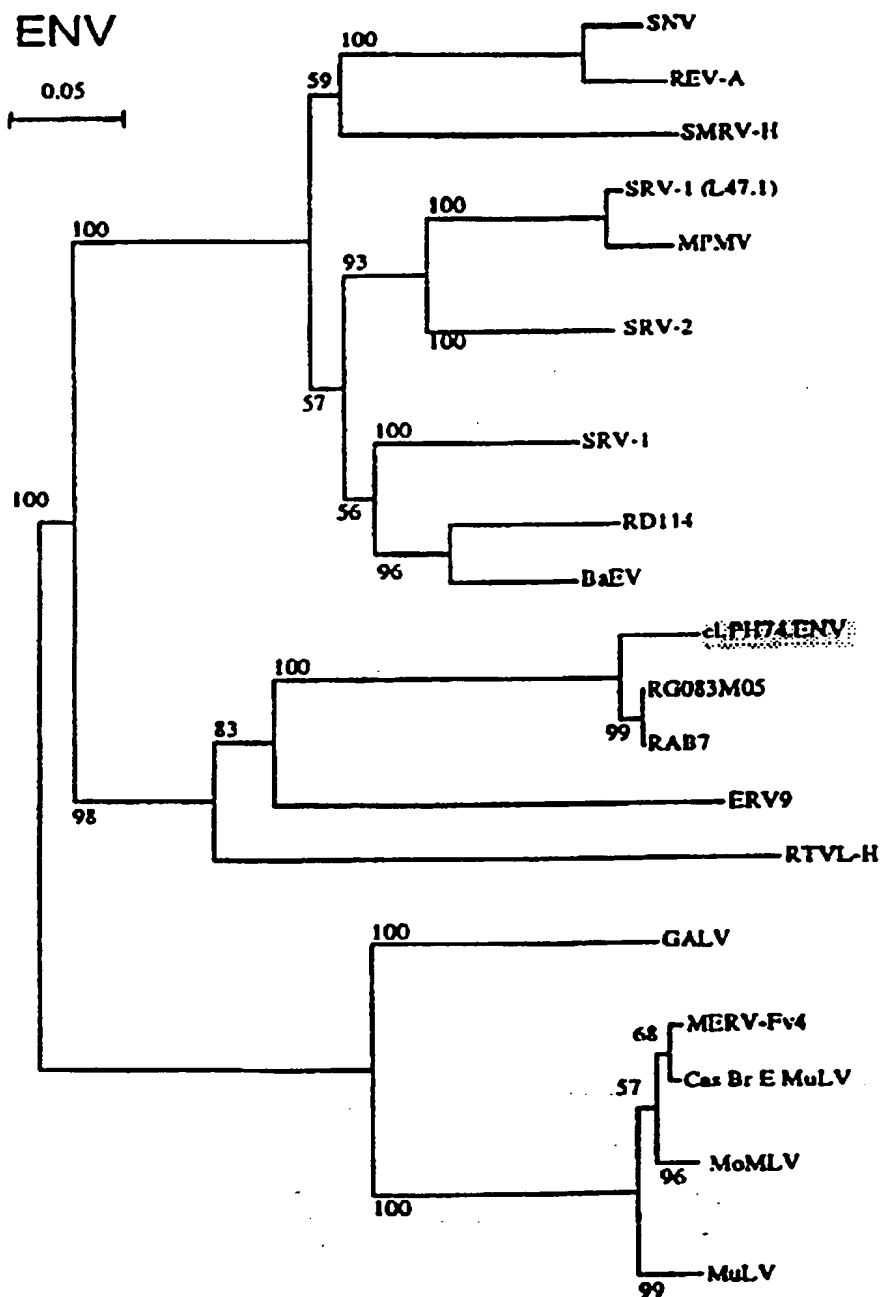


FIG 4C



09/446024-12169

FIG 5A

[illegible]

FIG 5B

5-RG-28000-28872
3-RG-37500-38314
5-6A2.1-600
5-PH74.1-530
5-24.4.1-486

Conclusions

[illegible]

5-RG-28000-28872
3-RG-37500-38314
5-6A2.1-600
5-PH74.1-530
5-24.4.1-486

Consensus

[illegible]

5-RG-28000-28972
3-RG-37500-38314
5-6A2.1-600
5-PH74.1-530
5-24.4.1-486

Consensus

CCATTCCTTGGAATCCGTGAGGCCAA-GAACTCCAGGTCAGAGAAATACGAGGCTTGCCACCAATCTTGGAAAGTGGTTCACACCAATCTTGGAAGCTCTTG
CCATTCCTTG-AMTCCATTAAGGCCAA-GAAATCCAGGTCAGAGAAATACGAGGCTTG-----CCACCAATCTTGGAAGCTCTTG
CCATTCCTTGGAATCCGTGAGGCCAA-GAACTCCAGGTCAGAGAAATACGAGGCTTGCCACCAATCTTGGAAAGTGGTTCACACCAATCTTGGAAGCTCTTG
CCATTCCTTGGAATCCGTGAGGCCAAAGCAATCTGATGAGGAAATACGAGGCTTGCCACCAATCTTGGAAAGTGGTTCACACCAATCTTGGAAGCTCTTG
CCATTCCTTGGAATCCGTGAGGCCAA-GAACTCCAGGTCAGAGAAATACGAGGCTTGCCACCAATCTTGGAAAGTGGTTCACACCAATCTTGGAAGCTCTTG
-----15-----
CCATTCCTTGGAATCCCTTARGSCAACCAATCTCAATCCAGGAAATACAGAGCTTGCCACCAATCTTGGAAAGTGGTTCACACCAATCTTGGAAGCTCTTG

5-RG-28000-28872
3-RG-37500-38314
5-6A2.1-600
5-PH74.1-530
5-24.4.1-486

Conclusions

873	TTAGCAGAGGACCCCCCGGTACACTTTTGGGCAACGACGAGCGAATCCA	
815	TTAGCAGAGGACCCCCCGGTACACTTTTGGGCAACGACGAGCGAATCCA	
600	TTAGCAGAGGACCCCCCGGTACACTTTTGGGCAACGACGAGCGAATCCA	
530	TTAGCAGAGGACCCCCCGGTACACTTTTGGGCAACGACGAGCGAATCCA	
486	TTAGCAGAGGACCCCCCGGTACACTTTTGGGCAACGACGAGCGAATCCA	
	TTAGCAGAGGACCCCCCGGTACACTTTTGGGCAACGACGAGCGAATCCA	
783	TTAGCAGAGGACCCCCCGGTACACTTTTGGGCAACGACGAGCGAATCCA	

ORF1: ENV (538 AA) FIG 6

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<--- L --->--- SU
MGLPYHIFLCVLSPCFTLTAPPPCRCMTSSSPHPEFLWRMQRPGNIDAPSYRSLSKGTP 60
A FT V S YQ C

TFTAHTHMPRNCYHSATLCMHANTHYWTGKMINPSCPGGLGVTVCWTFYFTQTGMSDGGGV 120

QDQAREKHVKEVISQLTGVTGTSPPYKGLDLSKLHETLRTHTRLVSLFNTTLTGLHEVSA 180
R

QNPTNCWICLPLNFRPYVSI PVPEQWNNPSTEINTTSVLVGPLVSNVEITHTSNLT CVKF 240
L

SNTTYTTNSQCIRWVTPPTQIVCLPSGIFFVCGTSAYRCLNGSSESMCFLSFLVPPMAIY 300
T

TEQDLYSYVISKPRNKRVPILPFVIGAGVLGALGTGIGGITTSTQFYKLSQELNGDMER 360

VADSLVTLQDQLNSLA AVLQNRALDLLTAERGGTCLFLGEECCYYVNQSGIVTEKVEE 420
R S K

IPDRIQRIAEELRNTGPWGLLSRWMPWILPFLGPLAAIILLLLFGPCIFDLLVNFVSSRI 480
R R Q N

EAVKLQMEPKMQSKTKIYRRPLDRPASPRSDVNDIKGTPPEEISAAQPLLRPNSAGSS 538

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ORF2 (52AA)

MEPKMQSKTKIYRRPLDRPVSPRSDVNDIKGTPPEEISAAQPLLRPNSAGSS-

Alignment ORF2 and Rex PLLV-L

```

ORF2          KIY-RRPLDRPASPRSDVNDIKGTPPEEISAAQPLLRP
++Y LD P SP ++ P S QPLLRP
Rex PTLV-L (B53482) RLYNTLSLDSPPSPPKELPA-----PSRFSPPQPLLRP

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ORF3 (48AA)

MLMTSKAPLLRKSQ LHNLYYAPIQQEAVRAVVGQPPQQLGFPVEMGD

Alignment ORF3 and Tat SIV-AGM

```

ORF3          MTSKAPLLRKSQ LHNLYYAPIQQEAVRAVVGQPPQ
+T AP R+ ++ +L AP+Q +++ G+ Q
Tat SIV-AGM(p05913) VTYHAPRTRRKKIRSLNLAPLQHSISTKWGRDQG

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